

09866020Results

SEQ ID NO: 1

SUMMARIES

Result	%		Query			ID	Description
	No.	Score	Match	Length	DB		
1	516	19.2	2273	4	US-09-177-650-88	Sequence 88, Appl	
2	510	18.9	2169	4	US-09-105-058C-22	Sequence 22, Appl	
3	465.4	17.3	896	4	US-09-105-058C-1	Sequence 1, Appli	
4	464	17.2	2814	4	US-09-177-650-90	Sequence 90, Appl	
5	460.8	17.1	2565	4	US-09-105-058C-26	Sequence 26, Appl	
6	460.8	17.1	2914	4	US-09-177-650-6	Sequence 6, Appli	
7	425	15.8	3287	4	US-09-105-058C-19	Sequence 19, Appl	
8	423.4	15.7	3232	4	US-09-177-650-1	Sequence 1, Appli	
9	423.4	15.7	3237	4	US-09-177-650-95	Sequence 95, Appl	
10	421.4	15.6	900	4	US-09-105-058C-3	Sequence 3, Appli	
11	420.6	15.6	900	4	US-09-105-058C-5	Sequence 5, Appli	
12	363.8	13.5	930	4	US-09-105-058C-17	Sequence 17, Appl	
13	334.2	12.4	735	4	US-09-105-058C-7	Sequence 7, Appli	
14	267.8	9.9	2028	4	US-09-634-920-1	Sequence 1, Appli	
15	267.8	9.9	3181	3	US-09-135-021-1	Sequence 1, Appli	
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RESULT 1

PCT-US01-09328-2

; Sequence 2, Application PC/TUS0109328

; GENERAL INFORMATION:

; APPLICANT: Jegla, Timothy James

; APPLICANT: ICAGEN, Inc.

; TITLE OF INVENTION: KCNQ5, a Novel Potassium Channel

; FILE REFERENCE: 018512-005010PC

; CURRENT APPLICATION NUMBER: PCT/US01/09328

; CURRENT FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: US 60/190,954

; PRIOR FILING DATE: 2000-03-21

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 2694

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: human outwardly-rectifying, voltage-gated

; OTHER INFORMATION: potassium channel KCNQ5-1 coding sequence

; NAME/KEY: CDS

; LOCATION: (1)..(2694)

; OTHER INFORMATION: KCNQ5-1

PCT-US01-09328-2

Query Match 100.0%; Score 2694; DB 1; Length 2694;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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SUMMARIES

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3	2689.2	99.8	3137	9	AF202977	AF202977 Homo sapi
4	2681.2	99.5	3074	6	AX253254	AX253254 Sequence
5	2681.2	99.5	3074	6	AX456864	AX456864 Sequence
6	2681.2	99.5	3074	9	AF249278	AF249278 Homo sapi
7	2625.2	97.4	2772	6	AX268474	AX268474 Sequence
8	2625.2	97.4	3111	6	AX268476	AX268476 Sequence
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11	963.4	35.8	1691	9	HSA272519	AJ272519 Homo sapi
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RESULT 1

AX322509

LOCUS AX322509 2694 bp DNA linear PAT 07-JAN-2002

DEFINITION Sequence 1 from Patent WO0192526.

ACCESSION AX322509

VERSION AX322509.1 GI:18093555

KEYWORDS .

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Dworetzky,S.I., Ramanathan,C.S., Trojnecki,J.T., Boissard,C.G. and Gribkoff,V.K.

TITLE Human kcnq5 potassium channel, methods and compositions thereof

JOURNAL Patent: WO 0192526-A 1 06-DEC-2001;

Bristol-Myers Squibb Company (US)

FEATURES Location/Qualifiers

source 1. .2694
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 714 a 671 c 669 g 640 t
ORIGIN

Query Match 100.0%; Score 2694; DB 6; Length 2694;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AF202977

LOCUS AF202977 3137 bp mRNA linear PRI 01-AUG-2000

DEFINITION Homo sapiens potassium voltage-gated channel, KQT-like subfamily,
member 5 (KCNQ5) mRNA, complete cds.

ACCESSION AF202977

VERSION AF202977.1 GI:7798695

KEYWORDS .

SOURCE Homo sapiens.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3137)

AUTHORS Schroeder,B.C., Hechenberger,M., Weinreich,F., Kubisch,C. and
Jentsch,T.J.

TITLE KCNQ5, a novel potassium channel broadly expressed in brain,
mediates M-type currents

J. Biol. Chem. 275 (31), 24089-24095 (2000)

MEDLINE 20379054

PUBMED 10816588

REFERENCE 2 (bases 1 to 3137)

AUTHORS Schroeder,B.C., Hechenberger,M., Weinreich,F., Kubisch,C. and
Jentsch,T.J.

TITLE Direct Submission

JOURNAL Submitted (09-NOV-1999) ZMNH, Hamburg University, Martinistrasse
85, Hamburg 20246, Germany

FEATURES Location/Qualifiers

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CDS 1. .2694

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subfamily, member 5"

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RESULT 6

AF249278

LOCUS AF249278 3074 bp mRNA linear PRI 02-AUG-2000
 DEFINITION Homo sapiens voltage-gated potassium channel (KCNQ5) mRNA, complete cds.

ACCESSION AF249278

VERSION AF249278.1 GI:9651966

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3074)

AUTHORS Lerche,C., Scherer,C.R., Seeborn,G., Derst,C., Wei,A.D., Busch,A.E. and Steinmeyer,K.

TITLE Molecular cloning and functional expression of KCNQ5, a potassium

Qy 361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCCTTTGGTTTGGAGTTC 420
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 Db 575 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCCTTTGGTTTGGAGTTC 634
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Qy 2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCCTCATGTCAAACCTGAAATAA 2694
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RESULT 15

AB000497

LOCUS AB000497 2827 bp mRNA linear ROD 23-JAN-1999

DEFINITION Mus musculus mRNA for alternative splicing:see accession between AB000494 and AB000504, complete cds.

ACCESSION AB000497

VERSION AB000497.1 GI:4176399

KEYWORDS mKQT2.4; alternative splicing.

SOURCE Mus musculus cDNA to mRNA.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (sites)

AUTHORS Nakamura,M., Watanabe,H., Kubo,Y., Yokoyama,M., Matsumoto,T., Sasai,H. and Nishi,Y.

TITLE KQT2, a new putative potassium channel family produced by alternative splicing. Isolation, genomic structure, and alternative splicing of the putative potassium channels

JOURNAL Recept. Channels 5 (5), 255-271 (1998)

MEDLINE 98330948

REFERENCE 2 (bases 1 to 2827)

AUTHORS Watanabe,H.

TITLE Direct Submission

JOURNAL Submitted (14-JAN-1997) Hirotaka Watanabe, Japan Tobacco, Inc., Pharmaceutical Basic Research Lab.; 6-2, Umegaoka, Aoba-ku, Yokohama, Kanagawa 227, Japan (E-mail:watanabe@ctrl.jti.co.jp, Tel:045-972-5741)

FEATURES Location/Qualifiers

source

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CDS

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polyA_site

2827
/note="20 a nucleotides"

BASE COUNT 589 a 830 c 816 g 592 t
ORIGIN

Query Match 19.3%; Score 519.6; DB 10; Length 2827;
Best Local Similarity 58.1%; Pred. No. 6.9e-123;
Matches 1042; Conservative 0; Mismatches 674; Indels 78; Gaps 4;

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Qy   604  CTACAGATCCTCCGCATGGTGCAGATGGACCGAAGGGGAGGCACTTGGAATTAAGGGT 663
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Db  753  TCGGTAGTCTACGCTCACAGCAAGGAGCTGGTGAAGTGCCTGGTACATTGGCTTCCTCTGC 812

Qy   724  CTTATTTTTCGTCCTTCTGCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTTCT 783
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SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2694	100.0	2694	22	AAS14652	Human cDNA encodin
2	2694	100.0	2694	24	AAD27192	Human potassium ch
3	2690.4	99.9	3071	22	AAS14651	Human cDNA for vol
4	2689.2	99.8	3137	22	AAC85414	Human KCNQ5 potass
5	2681.2	99.5	3074	22	AAH49499	Human KCNQ5 DNA.
6	2630	97.6	2667	22	AAS14653	Human cDNA encodin
7	2625.2	97.4	2772	22	AAH43633	Human ion-channel

8	2625.2	97.4	3111	22	AAH43634	Human ion-channel
9	2585	96.0	3718	21	AAC64371	Human KCNQ5 (KCN6q
10	963.4	35.8	125910	21	AAC64370	Human KCNQ5 (KCN6q
11	518.4	19.2	2335	21	AAA47618	KCNQ4 Potassium ch
12	516	19.2	2273	20	AAX57140	Mouse KCNQ2 cDNA.
13	510	18.9	2169	20	AAX26588	Nucleotide sequenc
14	480.6	17.8	7413	23	AAS74832	DNA encoding novel
15	477	17.7	2565	20	AAX81548	Human brain-derive
16	477	17.7	3195	23	AAS74831	DNA encoding novel
17	466.6	17.3	3029	20	AAX81547	Human brain-derive

RESULT 1

AAS14652

ID AAS14652 standard; cDNA; 2694 BP.

XX

AC AAS14652;

XX

DT 18-DEC-2001 (first entry)

XX

DE Human cDNA encoding a voltage gated potassium channel hKVNQ5-1.

XX

KW Human; ss; voltage-gated potassium channel; hKCNQ5-1; nootropic;

KW cerebroprotective; neurotropic; analgesic; vision disorder;

KW central nervous system disorder; epilepsy; migraine; hearing disorder;

KW psychotic disorder; seizure; learning disorder; memory disorder;

KW stroke; pain; gene therapy; splice variant.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS

1..2994

FT

/*tag= a

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/product= "hKCNQ5-1"

XX

PN WO200170759-A1.

XX

PD 27-SEP-2001.

XX

PF 20-MAR-2001; 2001WO-US09328.

XX

PR 21-MAR-2000; 2000US-190954P.

XX

PA (ICAG-) ICAGEN INC.

XX

PI Jegla TJ;

XX

DR WPI; 2001-611467/70.

DR

P-PSDB; AAU09020.

XX

PT Polypeptides and polynucleotides of potassium channel KCNQ5 for

PT identifying a compound modulating ion flux in eukaryotic cell or cell

PT membrane expressing the protein, comprises KCNQ alpha

PT subunits -

XX

PS Claim 5; Page 62-63; 78pp; English.

XX

CC The invention relates to an isolated polypeptide comprising an

CC alpha-subunit of a KCNQ potassium channel, with a subsequence having

CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid

CC sequence and forms a KCNQ potassium channel having the characteristic of

CC voltage-gating with at least an additional KCNQ alpha-subunit. Also

CC included in the scope of the invention are the nucleic acids encoding

CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),

CC expression vectors encoding them, antibodies against them, the use of

CC 3-dimensional computer modelling to identify molecules that bind to a

CC KCNQ containing potassium channel and modulate ion flux through the

CC channel. The KCNQ polypeptide is useful for identifying a compound that

CC increases or decreases ion flux through a potassium channel expressed in

CC an eukaryotic host cell or cell membrane. The compound (and the

CC KCNQ nucleic acid when used in gene therapy) is useful as
 CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
 CC such as disorders of the central nervous system, such as epilepsy,
 CC migraines, hearing and vision problems, psychotic disorders, seizures,
 CC learning and memory disorders, stroke and pain. The antibodies are
 CC useful for detecting a KCNQ5 polypeptide in a human tissue and the
 CC use of a nucleotide sequence of KCNQ5 to search computer databases to
 CC find variants of the sequence which are associated with disease states,
 CC is useful for screening mutations of KCNQ5. The present sequence is
 CC a splice variant of hKCNQ5 encoding hKCNQ5-1.
 XX
 SQ Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 other;

Query Match 100.0%; Score 2694; DB 22; Length 2694;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
 QY 61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGGTGGCCTG 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGGTGGCCTG 120

RESULT 2

AAD27192

ID AAD27192 standard; cDNA; 2694 BP.

XX

AC AAD27192;

XX

DT 09-APR-2002 (first entry)

XX

DE Human potassium channel polypeptide, KCNQ5 cDNA.

XX

KW Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;
 KW dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis;
 KW ALS; multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
 KW anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
 KW addiction; myokymia; Alzheimer's disease; age-associated memory loss;
 KW learning deficiency; cognitive disorder; motor disease; neuron disease;
 KW neurophysiological disorder; neuropsychological disorder; asthma;
 KW neuron cell death; brain tumour; gene therapy; antisense therapy;
 KW synaptic transmission; electrical excitability; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..2694

FT /*tag= a

FT /product= "Human KCNQ5 protein"

XX

PN WO200192526-A1.

XX

PD 06-DEC-2001.

XX

PF 24-MAY-2001; 2001WO-US17314.

XX

PR 26-MAY-2000; 2000US-207389P.

XX

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX

PI Dworetzky SI, Ramanathan CS, Trojnecki JT, Boissard CG;

PI Gribkoff VK;

XX

DR WPI; 2002-122069/16.

DR P-PSDB; AAE16599.

XX

Db 547 CTGGCTGCTGGTTCACAGGCAATGTCTTTGCCACATCTGCGCTTCGGAGCTTGC GGTTTC 606
 Qy 604 CTACAGATCCTCCGCATGGTGC GCATGGACCGAAGGGGAGGCACTTGGAAATTACTGGGT 663
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 607 TTGCAAATCTTGCGGATGATCCGTATGGACCGAGGGGTGGCACCTGGAAGCTCTTGGGA 666
 Qy 664 TCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTGGTT 723
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 667 TCGGTAGTCTACGCTCACAGCAAGGAGCTGGTGACTGCCTGGTACATTGGCTTCCTCTGC 726
 Qy 724 CTTATTTTTCGTCCTTCTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTTCT 783
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 Db 727 CTATCCTGGCCTCATTTCTGGTGTACTTGGCAGAAAAGGGTGAGAATGACCACCTTGAC 786
 Qy 784 ACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACCTATTGGCTATGGAGAC 843
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 787 ACCTACGCAGATGACTCTGGTGGGGTCTGATCACCTGACGACCATTGGCTACGGGGAC 846
 Qy 844 AAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGCATT 903
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 Db 847 AAGTACCTCAGACCTGGAACGGGAGGCTGCTGGCAGCGACCTTTACCTCATTGGTGTG 906
 Qy 904 TCTTCTTTGCACTTCTGCGGCATTCTTGGCTCAGGTTTGCATTAAAAGTACAAGAA 963
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 907 TCGTCTTTGCTCTTCCGGCTGGCATTTTGGGATCCGGCTTTGCCCTGAAAGTCCAAGAG 966
 Qy 964 CAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTAGTGT 1023
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 Db 967 CAGCATCGGCAAAAACACTTTGAGAAACGGCGGAACCTGCGGCAGGTCTGATCCAGTCT 1026
 Qy 1024 GTTTGGCGTAGTTACGCAGCTGAT----- 1047
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1027 GCCTGGAGATTCTATGCTACTAACCTCTCACGCACCGACCTGCACTCCACGTGGCAGTAC 1086
 Qy 1048 ---GAGAAATCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGACACCTGC 1104
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 Db 1087 TACGAGCGNACAGTCACTGTCCCATGTACAGCTCACAACTCAAACCTATGGGGCTCC 1146
 Qy 1105 AG-----CCCTACCAAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGCTAAGTTT 1159
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1147 AGACTCATCCACCTCTGAACCAGCTGGAGCTGTGAGGAATCTCAAGAGCAAATCTGGA 1206
 Qy 1160 AGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAG 1219
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 Db 1207 CTCACCTTCAGGAAGGAGCCACAGCCAGAGCCATCACCAAGCCCCGAGGCATGGCTGCC 1266
 Qy 1220 TAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGC----- 1256
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1267 AAGGGAAAGGGGTCTCCCCAGGCCAGACGGTCCGGCGGTCCCCAGTGCGGATCAGAGT 1326
 Qy 1257 --CGAGGGCAGTCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTC 1314
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1327 CTTGATGACAGCCCGAGCAAGGTGCCAAGAGCTGGAGCTTTGGTGACCGCAGCCGACA 1386
 Qy 1315 CGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACAGTGATAGATGCTGACACAGCC 1374
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1387 CGCCAGGCTTTCCGCATCAAGGGTGTGTCATCCCGGCAGAAATTCAGAAGAAGCAAGCCTC 1446
 Qy 1375 CTTGGCACTGATGATGATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGAAGAC 1434
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 Db 1447 CCTGGGGAGGACATCGTAGAGGACAACAAGAGCTGTAACCTGCGAGTTTGTGACTGAAGAT 1506
 Qy 1435 CTCACCCCACTTAAACTGTCTATTCGAGCTATCAGAATTATGAAATTTCTGTTGCA 1494
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 Db 1507 CTTACCCCTGGCCTCAAAGTYAGCATCAGAGCCGTGTGTGTATGCGGTTCTTGGTATCT 1566
 Qy 1495 AAACGGAAGTTTAAAGAAACGTTACGTCCATATGATGTAAAAGATGTCTTGAACAATAT 1554
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1567 AAGCGAAAGTTCAAAGAGAGTCTGCGCCCATATGATGTGATGGACGTCTCGAACAGTAC 1626
 Qy 1555 TCTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAA 1614

is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence: 37-71, >GC_rich#Low_complexity
Seq primer: M13 Forward
POLYA=No.

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                              /strain="C57BL/6J"
                              /db_xref="taxon:10090"
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                              /clone_lib="NIH_BMAP_M_S2"
                              /dev_stage="27-32 days"
                              /lab_host="DH10B (Life Technologies)"
                              /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M_S2 library is a subtracted library derived from
NIH_BMAP_M_S1, which in turn is a subtracted library
derived from a mixture of normalized libraries from ten
regions of the mouse brain (cerebellum, brain stems,
olfactory bulbs, hypothalamus, cortex, amygdala, basal
ganglia, pineal gland, striatum, hippocampus). The driver
used for subtraction consisted of a pool of 5,000 clones
from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
obtained from non-normalized and normalized mouse brain
spinal cord libraries.
TAG_LIB=NIH_BMAP_M_S2
TAG_TISSUE=corpus-striatum
TAG_SEQ=ACGGC"
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BASE COUNT 107 a 151 c 174 g 152 t
ORIGIN

Query Match 19.2%; Score 516.8; DB 10; Length 584;
Best Local Similarity 92.8%; Pred. No. 2.9e-116;
Matches 542; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

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Qy    47  CAGCCGCCAGGGGCGACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCG 106
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Db    1  CGGCCGCCAGGGGCGACGGCCTGCTGTTGCTCGGCACCCGCGCGCGCGCTCGGCGGAG 60

Qy    107 GCGGCGGTGGCCTGAGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGG 166
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    61 GCGGCGGCGGCTTGAGAGAGAGCCGCCGGGGCAAGCAGGGGGCCGAATGAGCCTGCTGG 120

Qy    167 GGAAGCCGCTCTCTTACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGG 226
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    121 GGAAGCCGCTCTCTTACACGAGTAGCCAGAGCTGTCGGCGCAACGTCAAGTACCGGCGGG 180

Qy    227 TGCAGAACTACCTGTACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTTCATCTACCACG 286
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    181 TGCAGAACTATCTGTACAACGTGCTGGAGCGACCCCGCGGCTGGGCGTTTCGTCTACCACG 240

Qy    287 CTTTCGTTTTTCTCCTTGCTTTGGTTGCTTGATTTTGTGAGTGTCTTACCATCCCTG 346
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    241 CGTTTCGTTTTTCTCCTTGCTTTGGTTGCTTGATTTTGTGAGTGTCTTACCATCCCTG 300

Qy    347 AGCACACAAAATTGGCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCT 406
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Db    301 AGCATACAAAATTGGCTTCAAGTTGCCTCTTAATTCTGGAGTTCGTGATGATCGTTGTCT 360

Qy    407 TTGGTTTGGAGTTCATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTGCGATATAGAGGAT 466
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    361 TTGGCTTGGAGTTCATCATTCGAATCTGGTCTGCGAGTTGCTGTTGTGCTGTATAGAGGAT 420

Qy    467 GGCAAGGAAGACTGAGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATGTTCTTA 526
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    421 GGCAAGGAAGACTGAGGTTTGCTCGAAACCATTCTGTGTAATAGATACCATGTTCTCA 480
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Qy 77 QNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVF 136
 Db 78 QNPLYNVLERPRGWAFIYHAYVFLLVFSCVLVSVFSTIKEYEKSSEGALYILEIVTIVVF 137

Qy 137 GLEFIIRIWSAGCCCRYRGWQGRRLRFARKPFCVIDTIVLIASIAVVSQAKTQGNIFATSAL 196
 Db 138 GVEYFVRIWAAGCCCRYRGWRGRLKFAKPFVCVIDIMVLIASIAVLAAGSQGNVFATSAL 197

Qy 197 RSLRFLQILRMVMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDA 256
 Db 198 RSLRFLQILRMIRMDRRGGTWKLLGSVVYAHSKELVTAWYIGFLCLILASFLVYLAEKGE 257

Qy 257 NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFA 316
 Db 258 NDHFDTYADALWWGLITLTTIGYGDKYPQTWNGRLLAATFTLIGVSFFALPAGILGSGFA 317

Qy 317 LKVQEQHRQKHFEKRRNPAANLIQCVWRSYAAD-----EKSVSIAATWK--PH 361
 Db 318 LKVQEQHRQKHFEKRRNPAAGLIQSAWRFYATNLSRTDLHSTWQYYERTVTVPMYRLIPP 377

Qy 362 LKALHTCSPTKKEQG-----EASSSQKLSFKERVMA SPRGQSIKSRQASVGD--R 410
 Db 378 LNQLELLRNLSKSKSLTFRKEPQPEPSPSQKVS LKDRV-FSSPRGMAAKGKSGPQAQTVR 436

Qy 411 RSPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRKSSQPKPVIDADTALGTDDVYDEKGC 470
 Db 437 RSPSADQSLDDSPSKVPSKWSFGDRSRTRQAFRIKGAASRQNSEASLP-GEDIVEDNKSC 495

Qy 471 QCDVSVEDLTPPLKTVIRAIRIMKPHVAKRKFKETLRPYDVKDIEQYSAGHLDMLCRIK 530
 Db 496 NCEFVTEDLTPGLKVSIRAVCVMRFLVSKRKFESLRPYDVMQIEQYSAGHLDMLSLRIK 555

Qy 531 SLQTRVDQILKGQITSDKKSREKITAETHETDLSMLGRVVKVEKQVQSIESKLDCLLD 590
 Db 556 SLQSRVDQIVGRGPTITD-KDRTKGPAETELPEDPSMMGRGLKVEKQVLSMEKKLDFLVS 614

Qy 591 IYQQVLRKGSASALALASFQIPPFEC-----EQTSQSPVDKDLSGSAQNSGC- 640
 Db 615 IYTQ--RMG-----IPPAETEAYFGAKEPEPAPPYHSPEDSRD---HADKHGCI 658

Qy 641 --LSRSTSANISRGLQFILTPNEFSAQTFFYALSPTMHSQATQVPISQS 686
 Db 659 IKIVRSTSS-----TGQRNYAAPPAL--PPAQCPSPTS 689

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	4588	100.0	897	22	AAU09020	Human voltage gate
2	4588	100.0	897	22	AAB47046	Human KCNQ5 potass
3	4588	100.0	897	23	AAE16599	Human potassium ch
4	4585	99.9	897	22	AAU09023	Human voltage gate
5	4585	99.9	897	22	AAU09025	Human voltage gate
6	4584	99.9	897	22	AAU09024	Human voltage gate
7	4582	99.9	897	22	AAU09022	Human voltage gate
8	4574	99.7	932	22	AAB86979	Human KCNQ5 protei
9	4527.5	98.7	888	22	AAU09021	Human voltage gate
10	4527.5	98.7	923	22	AAB47678	Human ion-channel
11	4330	94.4	846	21	AAB24241	Human KCNQ5 (KCN6q
12	1989.5	43.4	695	21	AAB01476	KCNQ4 Potassium ch
13	1989.5	43.4	695	23	AAE16621	Human potassium ch
14	1814.5	39.5	844	23	AAE16619	Human potassium ch
15	1813	39.5	722	20	AAY01530	Amino acid sequenc
16	1807.5	39.4	854	20	AAY23215	Human brain-derive
17	1807.5	39.4	912	22	ABG10644	Novel human diagno

RESULT 1
 AAU09020
 ID AAU09020 standard; Protein; 897 AA.
 XX
 AC AAU09020;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human voltage gated potassium channel hKVNQ5-1.
 XX
 KW Human; voltage-gated potassium channel; hKCNQ5-1; nootropic;
 KW cerebroprotective; neurotropic; analgesic; vision disorder;
 KW central nervous system disorder; epilepsy; migraine; hearing disorder;
 KW psychotic disorder; seizure; learning disorder; memory disorder;
 KW stroke; pain; gene therapy; splice variant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 343..640
 FT /label= Conserved_region
 FT /note= "This sequence is specifically claimed in
 FT claim 13"
 XX
 PN WO200170759-A1.
 XX
 PD 27-SEP-2001.
 XX
 PF 20-MAR-2001; 2001WO-US09328.
 XX
 PR 21-MAR-2000; 2000US-190954P.
 XX
 PA (ICAG-) ICAGEN INC.
 XX
 PI Jegla TJ;
 XX
 DR WPI; 2001-611467/70.
 DR N-PSDB; AAS14652.
 XX
 PT Polypeptides and polynucleotides of potassium channel KCNQ5 for
 PT identifying a compound modulating ion flux in eukaryotic cell or cell
 PT membrane expressing the protein, comprises KCNQ alpha
 PT subunits -
 XX
 PS Claim 17; Page 64; 78pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising an
 CC alpha-subunit of a KCNQ potassium channel, with a subsequence having
 CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
 CC sequence and forms a KCNQ potassium channel having the characteristic of
 CC voltage-gating with at least an additional KCNQ alpha-subunit. Also
 CC included in the scope of the invention are the nucleic acids encoding
 CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
 CC expression vectors encoding them, antibodies against them, the use of
 CC 3-dimensional computer modelling to identify molecules that bind to a
 CC KCNQ containing potassium channel and modulate ion flux through the
 CC channel. The KCNQ polypeptide is useful for identifying a compound that
 CC increases or decreases ion flux through a potassium channel expressed in
 CC an eukaryotic host cell or cell membrane. The compound (and the
 CC KCNQ nucleic acid when used in gene therapy) is useful as
 CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
 CC such as disorders of the central nervous system, such as epilepsy,
 CC migraines, hearing and vision problems, psychotic disorders, seizures,
 CC learning and memory disorders, stroke and pain. The antibodies are
 CC useful for detecting a KCNQ5 polypeptide in a human tissue and the
 CC use of a nucleotide sequence of KCNQ5 to search computer databases to
 CC find variants of the sequence which are associated with disease states,
 CC is useful for screening mutations of KCNQ5. The present sequence is
 CC encoded by a splice variant of hKCNQ5 and is hKCNQ5-1.
 XX

SQ Sequence 897 AA;

Query Match 100.0%; Score 4588; DB 22; Length 897;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MKDVESGRGRVLLNSAAARGDGLLLGTRAATLGGGGGLRESRRGKQGARMSLLGKPLS 60
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Db      1 MKDVESGRGRVLLNSAAARGDGLLLGTRAATLGGGGGLRESRRGKQGARMSLLGKPLS 60

Qy     61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVLLVFGCLILSVFSTIPEHTKL 120
      |||
Db     61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVLLVFGCLILSVFSTIPEHTKL 120

Qy    121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWGRLRFARKPFCVIDTIVLIASIA 180
      |||
Db    121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWGRLRFARKPFCVIDTIVLIASIA 180

Qy    181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
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Qy    241 VLIFSSFLVYLVEKDANKEFSTYADALWWTITLTTIGYDKTPTLWLGRLLSAGFALLG 300
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Qy    541 GKQGITSDKKSREKITAHEHTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600
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Qy    601 ASALALASFQIPPFCEQTS DYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660
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Db    601 ASALALASFQIPPFCEQTS DYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660

Qy    661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPLP 720
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Qy    721 AIKHLRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLT KD RSMRKS FDMGGETL 780
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Db    721 AIKHLRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLT KD RSMRKS FDMGGETL 780

Qy    781 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840
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Db    781 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840

Qy    841 VGPEETETDTFDAAPQ PAREAA FASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897
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Db    841 VGPEETETDTFDAAPQ PAREAA FASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897
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RESULT 2

AAB47046

ID AAB47046 standard; Protein; 897 AA.

XX

AC AAB47046;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE Human KCNQ5 potassium channel subunit.
 XX
 KW Human; KCNQ5; heteromeric channel; chromosome 6; Parkinson's disease;
 KW central nervous system; CNS; Alzheimer's disease; anxiety; ataxia;
 KW CNS damage; trauma; stroke; neurodegenerative illness; schizophrenia;
 KW compulsive behaviour; dementia; depression; Huntington's disease;
 KW mania; memory impairment; memory dysfunction; spinal cord damage;
 KW phobia; pick's disease; psychosis; stroke; tremor; seizure; convulsion;
 KW epilepsy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
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 FT Binding-site 120..138
 FT /label= Site 2
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 FT Binding-site 230..252
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 FT Binding-site 291..314
 FT /label= Site 6
 FT Domain 495..544
 FT /label= A-domain
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 PN WO200077035-A2.
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 PD 21-DEC-2000.
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 PF 29-MAY-2000; 2000WO-DK00289.
 XX
 PR 11-JUN-1999; 99DK-0000828.
 XX
 PA (NEUR-) NEUROSEARCH AS.
 XX
 PI Jentsch TJ;
 XX
 DR WPI; 2001-080678/09.
 DR N-PSDB; AAC85414.
 XX
 PT Novel genes encoding KCNQ5 potassium channel subunits, useful for
 PT treating Alzheimer's disease, anxiety, ataxia, stroke, dementia,
 PT depression, Huntington's disease, schizophrenia and Parkinson's disease
 PT -
 XX
 PS Claim 8; Page 48-50; 50pp; English.
 XX
 CC This sequence shows the human KCNQ5 protein. The KCNQ5 protein forms
 CC heteromeric channels with other KCNQ channel subunits, in particular
 CC KCNQ3 and KCNQ4. The KCNQ5 gene has been localised to the long arm of
 CC chromosome 6 (6q14). Chemicals which have the ability to bind to
 CC KCNQ5 are useful for diagnosis, treatment, prevention or alleviation
 CC of diseases related to diseases or adverse conditions of the central
 CC nervous system (CNS), including affective disorders, Alzheimer's
 CC disease, anxiety, ataxia, CNS damage caused by trauma, stroke or
 CC neurodegenerative illness, cognitive deficits, compulsive behavior,
 CC dementia, depression, Huntington's disease, mania, memory impairment,
 CC memory disorders, memory dysfunction, motion disorders, motor
 CC disorders, neurodegenerative diseases, Parkinson's disease and
 CC Parkinson-like motor disorders, phobias, pick's disease, psychosis,
 CC schizophrenia, spinal cord damage, stroke, tremor, seizures,
 CC convulsions and epilepsy.

XX
SQ Sequence 897 AA;

Query Match 100.0%; Score 4588; DB 22; Length 897;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MKDVESGRGRVLLNSAAARGDGLLLGTRAATLGGGGGLRESRRGKQGARMSLLGKPLS 60
      |||
Db      1 MKDVESGRGRVLLNSAAARGDGLLLGTRAATLGGGGGLRESRRGKQGARMSLLGKPLS 60

Qy     61 YTSSQSCRNVKYRRVQNYLYNVLERPRGWAFIYHAFVLLVFGCLILSVFSTIPEHTKL 120
      |||
Db     61 YTSSQSCRNVKYRRVQNYLYNVLERPRGWAFIYHAFVLLVFGCLILSVFSTIPEHTKL 120

Qy    121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLLRFARKPFCVIDTIVLIASIA 180
      |||
Db    121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLLRFARKPFCVIDTIVLIASIA 180

Qy    181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
      |||
Db    181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy    241 VLIFSSFLVYLVEKDANKEFSTYADALWGTITLTTIGYDKTPLTWLGRLLSAGFALLG 300
      |||
Db    241 VLIFSSFLVYLVEKDANKEFSTYADALWGTITLTTIGYDKTPLTWLGRLLSAGFALLG 300

Qy    301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCWRSYAADEKSVSIATWKP 360
      |||
Db    301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCWRSYAADEKSVSIATWKP 360

Qy    361 HLKALHTCSPTKKEQGEASSSQKLSFKERVMA SPRGQSIKSRQASVGDRRSPSTDITAE 420
      |||
Db    361 HLKALHTCSPTKKEQGEASSSQKLSFKERVMA SPRGQSIKSRQASVGDRRSPSTDITAE 420

Qy    421 GSPTKVQKSWSFNDRTRFRPSLRKSSQPKPVIDADTALGTDVYDEKGCQCDVSVEDLT 480
      |||
Db    421 GSPTKVQKSWSFNDRTRFRPSLRKSSQPKPVIDADTALGTDVYDEKGCQCDVSVEDLT 480

Qy    481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKD VIEQYSAGHLDMLCRIKSLQTRVDQIL 540
      |||
Db    481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKD VIEQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy    541 GKGQITSDKKSREKITA EHETDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600
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Db    541 GKGQITSDKKSREKITA EHETDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600

Qy    601 ASALALASFQIPPFCEQTS DYQSPVDSKDLGSAQNSGCLSRSTSANISRGLQFILT PN 660
      |||
Db    601 ASALALASFQIPPFCEQTS DYQSPVDSKDLGSAQNSGCLSRSTSANISRGLQFILT PN 660

Qy    661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPLP 720
      |||
Db    661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPLP 720

Qy    721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLT KD RSMRKS FDMGGETL 780
      |||
Db    721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLT KD RSMRKS FDMGGETL 780

Qy    781 LSVCPMPVKDLGKSLSVQN LIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840
      |||
Db    781 LSVCPMPVKDLGKSLSVQN LIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840

Qy    841 VGPEETETDTFDAAPQPARAAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897
      |||
Db    841 VGPEETETDTFDAAPQPARAAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897
```

RESULT 3

AAE16599

ID AAE16599 standard; Protein; 897 AA.

XX

AC AAE16599;

XX

DT 09-APR-2002 (first entry)

XX

DE Human potassium channel polypeptide, KCNQ5.

XX

KW Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;

KW dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis;

KW ALS; multiple sclerosis; MS; Parkinson's disease; ataxia; depression;

KW anxiety disorder; bipolar disorder; sleep disorder; eating disorder;

KW addiction; myokymia; Alzheimer's disease; age-associated memory loss;

KW learning deficiency; cognitive disorder; motor disease; neuron disease;

KW neurophysiological disorder; neuropsychological disorder; asthma;

KW neuron cell death; brain tumour; gene therapy; antisense therapy;

KW synaptic transmission; electrical excitability.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	Region	191..209
FT		/note= "Pore region"
FT	Region	265..285
FT		/note= "S4 voltage sensor region"

XX

PN WO200192526-A1.

XX

PD 06-DEC-2001.

XX

PF 24-MAY-2001; 2001WO-US17314.

XX

PR 26-MAY-2000; 2000US-207389P.

XX

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX

PI Dworetzky SI, Ramanathan CS, Trojnecki JT, Boissard CG;

PI Gribkoff VK;

XX

DR WPI; 2002-122069/16.

DR N-PSDB; AAD27192.

XX

PT Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding

PT it, for diagnosing, treating and identifying modulators useful in

PT treating neurological, neurophysiological and neuropsychological

PT diseases -

XX

PS Claim 25; Fig 2; 128pp; English.

XX

CC The invention relates to potassium channel polypeptides referred to

CC as KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5

CC polypeptides are useful for identifying compounds that modulate their

CC biological activity. The compounds identified and KCNQ5 polynucleotides

CC are useful for treating acute and chronic pain, migraine, acute stroke,

CC dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis

CC (ALS), multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety

CC disorders, depression, bipolar disorders, sleep disorders, eating

CC disorders, addiction, myokymia, Alzheimer's disease, age-associated

CC memory loss, learning deficiencies, cognitive disorders and motor

CC neuron diseases. The nucleic acid molecules of the invention are

CC further useful for treating neurophysiological, neuropsychological

CC disorders, asthma, neuron cell death and brain tumours. They are also

CC used in gene therapy and antisense therapy. KCNQ5 polypeptides modulate

CC synaptic transmission and electrical excitability in the brain and are

CC useful for generating antibodies. They are also useful to affinity

CC purify biological effectors from biological materials e.g. disease

CC tissues or cells. The present sequence is human KCNQ5 protein.

XX

SQ Sequence 897 AA;

Query Match 100.0%; Score 4588; DB 23; Length 897;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MKDVESGRGRVLLNSAAARGDGLLLGTRAATLGGGGGLRESRRGKQGARMSLLGKPLS 60
      |||
Db      1 MKDVESGRGRVLLNSAAARGDGLLLGTRAATLGGGGGLRESRRGKQGARMSLLGKPLS 60

Qy     61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVLLVFGCLILSVFSTIPEHTKL 120
      |||
Db     61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVLLVFGCLILSVFSTIPEHTKL 120

Qy    121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWGRLRFARKPFCVIDTIVLIASIA 180
      |||
Db    121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWGRLRFARKPFCVIDTIVLIASIA 180

Qy    181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
      |||
Db    181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy    241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
      |||
Db    241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300

Qy    301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
      |||
Db    301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360

Qy    361 HLKALHTCSPTKKEQGEASSSQKLSFKERVMA SPRGQSIKSRQASVGDRRSPSTDITAE 420
      |||
Db    361 HLKALHTCSPTKKEQGEASSSQKLSFKERVMA SPRGQSIKSRQASVGDRRSPSTDITAE 420

Qy    421 GSPTKVQKSWSFNDRTRFRPSRLRKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480
      |||
Db    421 GSPTKVQKSWSFNDRTRFRPSRLRKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480

Qy    481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKD VIEQYSAGHLDMLCRIKSLQTRVDQIL 540
      |||
Db    481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKD VIEQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy    541 GKGQITSDKKSREKITA EHETDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600
      |||
Db    541 GKGQITSDKKSREKITA EHETDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600

Qy    601 ASALALASFQIPPFCEQTS DYQSPVDSKDLGSAQNSGCLSRSTSANISRGLQFILT PN 660
      |||
Db    601 ASALALASFQIPPFCEQTS DYQSPVDSKDLGSAQNSGCLSRSTSANISRGLQFILT PN 660

Qy    661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPLP 720
      |||
Db    661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPLP 720

Qy    721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLT KDRSMRKS FDMGGETL 780
      |||
Db    721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLT KDRSMRKS FDMGGETL 780

Qy    781 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840
      |||
Db    781 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840

Qy    841 VGPEETETDTFDAAPQ PAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897
      |||
Db    841 VGPEETETDTFDAAPQ PAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897
```

RESULT 15
AA01530
ID AAY01530 standard; Protein; 722 AA.

```

XX AC AAY01530;
XX XX
XX DT 16-JUN-1999 (first entry)
XX XX
XX DE Amino acid sequence of murine KCNQ2/KvLRL1.
XX KW KCNQ protein; nervous system-specific potassium channel;
KW neuronal excitability; neurotransmitter release; KCNQ modulator;
KW ataxia; myokymia; seizure; Alzheimer's disease; Parkinson's disease;
KW age-associated memory loss; learning deficiency; motor neuron disease;
KW epilepsy; stroke.
XX OS Mus sp.
XX PN WO9907832-A1.
XX PD 18-FEB-1999.
XX PF 26-JUN-1998; 98WO-US13276.
XX PR 12-AUG-1997; 97US-0055599.
XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX PI Blanar MA, Dworetzky S, Gribkoff VK, Levesque PC;
PI Little WA, Neubauer MG, Yang W;
XX DR WPI; 1999-190047/16.
DR N-PSDB; AAX26588.
XX PT New potassium channels, KCNQ2 and KCNQ3 - may be involved in
PT neurotransmission and neuroprotection, used to treat, e.g. ataxia
XX PS Claim 4; Fig 10A-D; 64pp; English.
XX CC The present sequence represents murine KCNQ2/KvLRL1. KCNQ proteins are
CC nervous system-specific potassium channels. In neurons, potassium
CC channels regulate neuronal excitability, action potential shape
CC and firing pattern, and neurotransmitter release. KCNQ modulators
CC may be used to treat disorders such as ataxia, myokymia, seizures,
CC Alzheimer's disease, Parkinson's disease, age-associated memory
CC loss, learning deficiencies, motor neuron diseases, epilepsy, and
CC stroke.
XX SQ Sequence 722 AA;

Query Match 39.5%; Score 1813; DB 20; Length 722;
Best Local Similarity 55.5%; Pred. No. 2e-152;
Matches 393; Conservative 72; Mismatches 153; Indels 90; Gaps 17;

Qy 17 AARGDGLLLGTRAAATLGGGGGGLRESRRRGKQGARMSLLGKPLSYTSSQSCRRNVKYRRV 76
   : | ||: |: | | | : | | || | | :|| ||::
Db 34 STRDGALLIAGSEAPK---RGSVLSPRTGGAGA-----GKP-----PKRNAFYRK 77

Qy 77 QNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVF 136
   ||:||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 78 QNFLYNVLERPRGWAFIYHAYVFLLVFSCLVLSVFSTIKEYEKSSEGALYILEIVTIVVF 137

Qy 137 GLEFIIRIWASGCCCRYGRGWQRLRFARKPFCVIDITVLIASIAVVSAKTQGNIFATSAL 196
   ||::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 138 GVEYFVRIWAAGCCCRYGRWGRGLKFARKPFCVIDIMVLIASIAVLAAQSQQNVFATSAL 197

Qy 197 RSLRFLQLIRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDA 256
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 198 RSLRFLQLIRMIRMDRRGGTWKLLGSVVYAHSKELVTAWYIGFLCLILASFVYLAEKEGE 257

Qy 257 NKEFSTYADALWWGTITLTITIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFA 316
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 258 NDHFDTYADALWWGLITLTITIGYGDKYPOTWNGRLLAATFTLIGVSFFALPAGILGSGFA 317

```


Qy 77 QNYLYNVLERPRGWAFIYHAFVLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVF 136
 Db 78 QNFLYNVLERPRGWAFIYHAYVLLVFSCLVLSVFSTIKEYKSSEALYILEIVTIVVF 137

Qy 137 GLEFIIRIWSAGCCCRYRGWQGRRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSAL 196
 Db 138 GVEYFVRIVAAGCCCRYRGWRGLKFARKPFCVIDIMVLIASIAVLAAGSQGNVFATSAL 197

Qy 197 RSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDA 256
 Db 198 RSLRFLQILRMIRMDRRGGTWKLLGSVVYAHSKELVTAWYIGFLCLILASFLVYLAEKGE 257

Qy 257 NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFA 316
 Db 258 NDHFDTYADALWWGLITLTTIGYGDKYPQTWNGRLLAATFTLIGVSFFALPAGILGSGFA 317

Qy 317 LKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSI-ATWK 359
 Db 318 LKVQEQHRQKHFEKRRNPAAGLIQSAWRFYATNLSRTDLHSTWQ 361

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4588	100.0	897	1	CIQ5_HUMAN	Q9nr82 homo sapien
2	4288	93.5	878	1	CIQ5_MOUSE	Q9jk45 mus musculu
3	1989.5	43.4	695	1	CIQ4_HUMAN	P56696 homo sapien
4	1826	39.8	852	1	CIQ2_RAT	O88943 rattus norv
5	1795.5	39.1	872	1	CIQ2_HUMAN	O43526 homo sapien
6	1776.5	38.7	759	1	CIQ2_MOUSE	Q9z351 mus musculu
7	1611	35.1	872	1	CIQ3_HUMAN	O43525 homo sapien
8	1577	34.4	873	1	CIQ3_RAT	O88944 rattus norv
9	1571	34.2	866	1	CIQ3_BOVIN	P58126 bos taurus
10	1102.5	24.0	676	1	CIQ1_HUMAN	P51787 homo sapien
11	1100	24.0	604	1	CIQ1_MOUSE	P97414 mus musculu

RESULT 1

CIQ5_HUMAN

ID CIQ5_HUMAN STANDARD; PRT; 897 AA.
 AC Q9NR82; Q9NRN0; Q9NYA6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Voltage-gated potassium channel protein KQT-like 5.
 GN KCNQ5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=20357367; PubMed=10787416;
 RA Lerche C., Scherer C.R., Seebohm G., Derst C., Wei A.D., Busch A.E.,
 RA Steinmeyer K.;
 RT "Molecular cloning and functional expression of KCNQ5, a potassium
 RT channel subunit that may contribute to neuronal M-current
 RT diversity."
 RL J. Biol. Chem. 275:22395-22400(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RC TISSUE=Brain;
 RX MEDLINE=20379054; PubMed=10816588;
 RA Schroeder B.C., Hechenberger M., Weinreich F., Kubisch C.,
 RA Jentsch T.J.;

RT "KCNQ5, a novel potassium channel broadly expressed in brain, mediates
RT M-type currents.";
RL J. Biol. Chem. 275:24089-24095(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Kananura C., Biervert B., Hechenberger M., Engels H., Steinlein O.K.;
RT "The new voltage gated potassium channel KCNQ5 and early infantile
RT convulsions.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE OF 37-897 FROM N.A. (ISOFORM 1).
RC TISSUE=Brain, and Retina;
RA Kniazeva M., Han M.;
RT "A new gene of the voltage-gated potassium channel KCNQ family, KCNQ5,
RT is a candidate gene for retinal disorders.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP CHARACTERIZATION, AND ACTIVATION BY RETICABINE.
RX MEDLINE=21095345; PubMed=11159685;
RA Wickenden A.D., Zou A., Wagoner P.K., Jegla T.;
RT "Characterization of KCNQ5/Q3 potassium channels expressed in
RT mammalian cells.";
RL Br. J. Pharmacol. 132:381-384(2001).
CC -!- FUNCTION: PROBABLY IMPORTANT IN THE REGULATION OF NEURONAL
CC EXCITABILITY. ASSOCIATES WITH KCNQ3 TO FORM A POTASSIUM CHANNEL
CC WHICH CONTRIBUTES TO M-TYPE CURRENT, A SLOWLY ACTIVATING AND
CC DEACTIVATING POTASSIUM CONDUCTANCE WHICH PLAYS A CRITICAL ROLE IN
CC DETERMINING THE SUBTHRESHOLD ELECTRICAL EXCITABILITY OF NEURONS.
CC MAY CONTRIBUTE, WITH OTHER POTASSIUM CHANNELS, TO THE MOLECULAR
CC DIVERSITY OF AN HETEROGENEOUS POPULATION OF M-CHANNELS, VARYING IN
CC KINETIC AND PHARMACOLOGICAL PROPERTIES, WHICH UNDERLY THIS
CC PHYSIOLOGICALLY IMPORTANT CURRENT. INSENSITIVE TO
CC TETRAETHYLAMMONIUM, BUT INHIBITED BY BARIUM, LINOPIRIDINE AND
CC XE991. ACTIVATED BY NIFLUMIC ACID AND THE ANTICONVULSANT
CC RETIGABINE. MUSCARINE SUPPRESSES KCNQ5 CURRENT IN XENOPUS OOCYTES
CC IN WHICH CLONED KCNQ5 CHANNELS WERE COEXPRESSED WITH M(1)
CC MUSCARINIC RECEPTORS.
CC -!- SUBUNIT: HETEROMULTIMER WITH KCNQ3.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; ISOFORM 1 (SHOWN HERE), 2 AND 3;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN BRAIN AND SKELETAL
CC MUSCLE. IN BRAIN, EXPRESSED IN CEREBRAL CORTEX, OCCIPITAL POLE,
CC FRONTAL LOBE AND TEMPORAL LOBE. LOWER LEVELS IN HIPPOCAMPUS AND
CC PUTAMEN. LOW TO UNDETECTABLE LEVELS IN MEDULLA, CEREBELLUM AND
CC THALAMUS.
CC -!- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KQT
CC SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF249278; AAF91335.1; ALT_INIT.
DR EMBL; AF202977; AAF69797.1; -.
DR EMBL; AJ272506; CAC88112.1; -.
DR EMBL; AJ272507; CAC88112.1; JOINED.
DR EMBL; AJ272508; CAC88112.1; JOINED.
DR EMBL; AJ272509; CAC88112.1; JOINED.
DR EMBL; AJ272510; CAC88112.1; JOINED.
DR EMBL; AJ272511; CAC88112.1; JOINED.
DR EMBL; AJ272512; CAC88112.1; JOINED.
DR EMBL; AJ272513; CAC88112.1; JOINED.
DR EMBL; AJ272514; CAC88112.1; JOINED.

DR EMBL; AJ272515; CAC88112.1; JOINED.
 DR EMBL; AJ272516; CAC88112.1; JOINED.
 DR EMBL; AJ272517; CAC88112.1; JOINED.
 DR EMBL; AJ272518; CAC88112.1; JOINED.
 DR EMBL; AJ272519; CAC88112.1; JOINED.
 DR EMBL; AF263835; AAF73446.1; -.
 DR HSSP; Q54397; 1BL8.
 DR Genew; HGNC:6299; KCNQ5.
 DR InterPro; IPR001622; K+channel_pore.
 DR InterPro; IPR003946; KCNQ1_channel.
 DR InterPro; IPR003091; K_channel.
 DR InterPro; IPR000636; M+channel_nlg.
 DR Pfam; PF00520; ion_trans; 1.
 DR Pfam; PF03520; KCNQ1_channel; 1.
 DR PRINTS; PR00169; KCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Multigene family; Alternative splicing.
 FT TRANSMEM 91 111 SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 122 142 SEGMENT S2 (POTENTIAL).
 FT TRANSMEM 166 186 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 195 217 SEGMENT S4 (POTENTIAL).
 FT TRANSMEM 232 252 SEGMENT S5 (POTENTIAL).
 FT DOMAIN 264 284 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
 FT TRANSMEM 291 311 SEGMENT S6 (POTENTIAL).
 FT VARSPLIC 372 381 KKEQGEASSS -> N (IN ISOFORM 2).
 FT VARSPLIC 372 381 KKEQGEASSS -> NKFCSNKQKLFRMYTSRKQS (IN
 ISOFORM 3).
 FT CONFLICT 57 58 KP -> SR (IN REF. 1).
 FT CONFLICT 94 94 Y -> H (IN REF. 4).
 FT CONFLICT 692 692 A -> V (IN REF. 4).
 FT CONFLICT 764 764 T -> P (IN REF. 4).
 FT CONFLICT 822 822 S -> R (IN REF. 4).
 FT CONFLICT 874 874 R -> Q (IN REF. 4).
 SQ SEQUENCE 897 AA; 99024 MW; 0FD7C7731C1D8D11 CRC64;

 Query Match 100.0%; Score 4588; DB 1; Length 897;
 Best Local Similarity 100.0%; Pred. No. 1.6e-254;
 Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 MKDVESGRVLLNSAAARGDGLLLGTRAATLGGGGGLRESRRGKQGARMSSLLGKPLS 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MKDVESGRVLLNSAAARGDGLLLGTRAATLGGGGGLRESRRGKQGARMSSLLGKPLS 60

 Qy 61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVLLVFGCLILSVFSTIPEHTKL 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVLLVFGCLILSVFSTIPEHTKL 120

 Qy 121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWGRLRFARKPFCVIDTIVLIASIA 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWGRLRFARKPFCVIDTIVLIASIA 180

 Qy 181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

 Qy 241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTITIGYDKTPLTWLGRLLSAGFALLG 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTITIGYDKTPLTWLGRLLSAGFALLG 300

 Qy 301 ISFFALPAGILGSGFALKVQEQRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 ISFFALPAGILGSGFALKVQEQRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360

 Qy 361 HLKALHTCSPTKKEQGEASSSQLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 HLKALHTCSPTKKEQGEASSSQLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420

 Qy 421 GSPTKVQKSWSFNDRTRFRPSLRKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 GSPTKVQKSWSFNDRTRFRPSLRKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480

Qy 481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 541 GKQQTSDKKSREKITAETHETDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 541 GKQQTSDKKSREKITAETHETDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 601 ASALALASFQIPPFCEQTSYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 601 ASALALASFQIPPFCEQTSYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPPL 720
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPPL 720
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 781 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 781 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 841 VGPEETETDTFDAAPQFAFAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 841 VGPEETETDTFDAAPQFAFAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 3

CIQ4_HUMAN

ID CIQ4_HUMAN STANDARD; PRT; 695 AA.
 AC P56696; O96025;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Voltage-gated potassium channel protein KQT-like 4.
 GN KCNQ4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANT DFNA2 SER-285.
 RC TISSUE=Retina;
 RX MEDLINE=99148276; PubMed=10025409;
 RA Kubisch C., Schroeder B.C., Friedrich T., Luetjohann B.,
 RA El-Amraoui A., Marlin S., Petit C., Jentsch T.J.;
 RT "KCNQ4, a novel potassium channel expressed in sensory outer hair
 RT cells, is mutated in dominant deafness.";
 RL Cell 96:437-446(1999).
 RN [2]
 RP INHIBITION BY M1 MUSCARINIC RECEPTORS.
 RX MEDLINE=20178300; PubMed=10713961;
 RA Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Jentsch T.J.,
 RA Brown D.A.;
 RT "Inhibition of KCNQ1-4 potassium channels expressed in mammalian cells
 RT via M1 muscarinic acetylcholine receptors.";
 RL J. Physiol. (Lond) 522:349-355(2000).
 RN [3]
 RP PHARMACOLOGICAL CHARACTERIZATION, AND POSSIBLE FUNCTION.
 RX MEDLINE=21143874; PubMed=11245603;
 RA Soegaard R., Ljungstroem T., Pedersen K.A., Olesen S.-P.,
 RA Jensen B.S.;
 RT "KCNQ4 channels expressed in mammalian cells: functional
 RT characteristics and pharmacology.";
 RL Am. J. Physiol. 280:C859-C866(2001).
 RN [4]
 RP VARIANTS DFNA2 SER-276; CYS-285 AND SER-321.
 RX MEDLINE=99299248; PubMed=10369879;

RA Coucke P.J., Van Hauwe P., Kelley P.M., Kunst H., Schattelman I.,
 RA Van Velzen D., Meyers J., Ensink R.J., Verstreken M., Declau F.,
 RA Marres H., Kastury K., Bhasin S., McGuirt W.T., Smith R.J.H.,
 RA Cremers C.W.R.J., Van de Heyning P., Willems P.J., Smith S.D.,
 RA Van Camp G.;
 RT "Mutations in the KCNQ4 gene are responsible for autosomal dominant
 RT deafness in four DFNA2 families.";
 RL Hum. Mol. Genet. 8:1321-1328(1999).
 RN [5]
 RP VARIANT DFNA2 SER-281.
 RX MEDLINE=20040027; PubMed=10571947;
 RA Talebizadeh Z., Kelley P.M., Askew J.W., Beisel K.W., Smith S.D.;
 RT "Novel mutation in the KCNQ4 gene in a large kindred with dominant
 RT progressive hearing loss.";
 RL Hum. Mutat. 14:493-501(1999).
 RN [6]
 RP VARIANT DFNA2 HIS-274.
 RX MEDLINE=20388752; PubMed=10925378;
 RA Van Hauwe P., Coucke P.J., Ensink R.J., Huygen P., Cremers C.W.R.J.,
 RA Van Camp G.;
 RT "Mutations in the KCNQ4 K+ channel gene, responsible for autosomal
 RT dominant hearing loss, cluster in the channel pore region.";
 RL Am. J. Med. Genet. 93:184-187(2000).
 CC -!- FUNCTION: PROBABLY IMPORTANT IN THE REGULATION OF NEURONAL
 CC EXCITABILITY. MAY UNDERLIE A POTASSIUM CURRENT INVOLVED IN
 CC REGULATING THE EXCITABILITY OF SENSORY CELLS OF THE COCHLEA. KCNQ4
 CC CHANNELS ARE BLOCKED BY LINOPIRDIN, XE991 AND BEPRIDIL, WHEREAS
 CC CLOFILIMUM IS WITHOUT SIGNIFICANT EFFECT. MUSCARINIC AGONIST
 CC OXOTREMORINE-M STRONGLY SUPPRESS KCNQ4 CURRENT IN CHO CELLS IN
 CC WHICH CLONED KCNQ4 CHANNELS WERE COEXPRESSED WITH M1 MUSCARINIC
 CC RECEPTORS.
 CC -!- SUBUNIT: MAY FORM HETEROMULTIMERS WITH KCNQ3.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SITUATED AT THE
 CC BASAL MEMBRANE OF COCHLEAR OUTER HAIR CELLS (BY SIMILARITY).
 CC -!- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE OUTER, BUT NOT THE INNER,
 CC SENSORY HAIR CELLS OF THE COCHLEA. SLIGHTLY EXPRESSED IN HEART,
 CC BRAIN AND SKELETAL MUSCLE.
 CC -!- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION (BY SIMILARITY).
 CC -!- DISEASE: DEFECTS IN KCNQ4 ARE A CAUSE OF NONSYNDROMIC
 CC SENSORINEURAL DEAFNESS TYPE 2 (DFNA2), AN AUTOSOMAL DOMINANT FORM
 CC OF PROGRESSIVE HEARING LOSS.
 CC -!- MISCELLANEOUS: MUTAGENESIS EXPERIMENTS WERE CARRIED OUT BY
 CC EXPRESSING IN XENOPUS OOCYTES KCNQ4 MUTANTS EITHER INDIVIDUALLY
 CC (HOMOMULTIMERS) OR IN COMBINATION WITH WILD-TYPE KCNQ4 (MUT/WT
 CC HOMOMULTIMERS) IN A RATIO OF 1:1, TO MIMIC THE SITUATION IN A
 CC HETEROZYGOUS DFNA2 PATIENT.
 CC -!- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KQT
 CC SUBFAMILY.
 CC -!- DATABASE: NAME=Hereditary hearing loss homepage;
 CC NOTE=Gene page;
 CC WWW="http://www.uia.ac.be/dnalab/hhh/hhhgenes.html".
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF105202; AAD14680.1; -.
 DR EMBL; AF105216; AAD14681.1; -.
 DR EMBL; AF105203; AAD14681.1; JOINED.
 DR EMBL; AF105204; AAD14681.1; JOINED.
 DR EMBL; AF105205; AAD14681.1; JOINED.
 DR EMBL; AF105206; AAD14681.1; JOINED.
 DR EMBL; AF105207; AAD14681.1; JOINED.

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DR EMBL; AF105208; AAD14681.1; JOINED.
DR EMBL; AF105209; AAD14681.1; JOINED.
DR EMBL; AF105210; AAD14681.1; JOINED.
DR EMBL; AF105211; AAD14681.1; JOINED.
DR EMBL; AF105212; AAD14681.1; JOINED.
DR EMBL; AF105213; AAD14681.1; JOINED.
DR EMBL; AF105214; AAD14681.1; JOINED.
DR EMBL; AF105215; AAD14681.1; JOINED.
DR HSSP; Q54397; 1BL8.
DR Genew; HGNC:6298; KCNQ4.
DR MIM; 603537; -.
DR MIM; 600101; -.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003946; KCNQ1_channel.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR000636; M+channel_nlg.
DR Pfam; PF00520; ion_trans; 1.
DR Pfam; PF03520; KCNQ1_channel; 1.
DR PRINTS; PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Multigene family; Disease mutation; Deafness; Alternative splicing.
FT TRANSMEM 98 118 SEGMENT S1 (POTENTIAL).
FT TRANSMEM 132 152 SEGMENT S2 (POTENTIAL).
FT TRANSMEM 173 193 SEGMENT S3 (POTENTIAL).
FT TRANSMEM 202 224 SEGMENT S4 (POTENTIAL).
FT TRANSMEM 238 258 SEGMENT S5 (POTENTIAL).
FT DOMAIN 271 292 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
FT TRANSMEM 297 317 SEGMENT S6 (POTENTIAL).
FT VARSPLIC 378 431 MISSING (IN ISOFORM 2).
FT VARIANT 274 274 L -> H (IN DFNA2).
FT /FTId=VAR_010936.
FT VARIANT 276 276 W -> S (IN DFNA2).
FT /FTId=VAR_008726.
FT VARIANT 281 281 L -> S (IN DFNA2).
FT /FTId=VAR_010937.
FT VARIANT 285 285 G -> C (IN DFNA2; LOSS OF POTASSIUM
FT SELECTIVITY OF THE PORE).
FT /FTId=VAR_008727.
FT VARIANT 285 285 G -> S (IN DFNA2).
FT /FTId=VAR_001547.
FT VARIANT 321 321 G -> S (IN DFNA2).
FT /FTId=VAR_008728.
FT MUTAGEN 285 285 G->S: NO CURRENT (HOMOMULTIMERS); 90% WT
FT CURRENT REDUCTION (MU/WT HOMOMULTIMERS).
SQ SEQUENCE 695 AA; 77091 MW; A58737BD845E1A3A CRC64;

Query Match 43.4%; Score 1989.5; DB 1; Length 695;
Best Local Similarity 60.5%; Pred. No. 2.3e-106;
Matches 412; Conservative 76; Mismatches 104; Indels 89; Gaps 13;

Qy 35 GGGGGLRESRRGKQGARMSSLLGKPL-----SYTSSQSCRRNVKYRRVQNYL 80
| | | | | : | | | | | : | | | | | : | | | | | :
Db 37 GGGGSPR-----RLGLLGSPLPPGAPLPGPGSGSGSACGQRSSAAHKRYRRLQN WV 87

Qy 81 YNVLERPRGWAFIYHAFVLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEY 140
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 88 YNVLERPRGWAFVYHVFIFFLLVFSLVSLSTIQEHQELANECCLLILEFVMIVVFGLEY 147

Qy 141 IIRIWSAGCCCRYRGWQGRFRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLR 200
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 148 IVRVWSAGCCCRYRGWQGRFRFARKPFCVIDFIVFVASVAVIAAGTQGNIFATSALRSMR 207

Qy 201 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKEF 260
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 208 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFASFLVYLAEKDANSDF 267

Qy 261 STYADALWGWTTITLTITIGYDKTPTLTLWGRLLSAGFALLGISFFALPAGILGSGFALKVQ 320
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 268 SSYADSLWGWTTITLTITIGYDKTPTHTWLGRVLAAGFALLGISFFALPAGILGSGFALKVQ 327

Qy 321 EQHRQKHFEKRRNPAANLIQCVRWSYAAD-EKSVSIATW----- 358

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Db 328 EQHRQKHFEKRRMPAANLIQAARLYSTDMRAYLTATWYYYDSILPSFRELALLFEHVQ 387
Qy 359 -----KPHLKALHTCSPTKKEQGEASSSQKLSFKERVMS 394
Db 388 RARNGGLRPLEVRRAPVDPGAPSRYPVATCHRPGSTSFCPGESS---RMGIKDRIRMG 444
Qy 395 PRGQSIKSRQ--ASVGDRRSPSTDITAEG-SPTKVQKSWSFNDRTFRPSLRLKSSQPKP 451
Db 445 SQRRTGPSKQQLAPPTMPTSPSSEQVGEATSPTKVQKSWSFNDRTFRASLRL-----KP 499
Qy 452 VIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDV 511
Db 500 RTSAEDA-PSEEVAAEKSYQCELTVDIMPVKTVIRSIRILKFLVAKRKFKETLRPYDV 558
Qy 512 KDVIEWEYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSRE--KITAEHETDSDLML 568
Db 559 KDVIEWEYSAGHLDMLGRIKSLQTRVDQIVGRG--PGDRKAREKGDGKPSDAEVVDEISMM 616
Qy 569 GRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPECEQTSQSDYQSPVDS 628
Db 617 GRVVKVEKQVQSIEHKLDDLGLFYRCLRSCTSA--SLGAVQVPLFDPDITSQSDYHSPVDH 674
Qy 629 KDLSGSAQNSGCLSRSTSANI 649
Db 675 EDISVSAQTLIS-ISRSTVSTNM 694

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SUMMARIES

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	1831	39.9	842	11	Q923N2 mus musculu
2	1815.5	39.6	723	11	Q923N4 mus musculu
3	1810	39.5	870	11	Q8r498 mus musculu
4	1792	39.1	840	11	Q923N1 mus musculu
5	1787.5	39.0	759	11	Q923N5 mus musculu
6	1755.5	38.3	747	11	Q923N6 mus musculu
7	1634.5	35.6	623	11	Q923N0 mus musculu
8	1633.5	35.6	570	11	Q923N3 mus musculu
9	1230.5	26.8	473	11	Q923M9 mus musculu
10	1220.5	26.6	692	5	Q967F8 caenorhabdi
11	1197	26.1	347	11	Q923M7